

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/446,915TEAM 6
#12
MB
10/23/96DATE: 07/11/95
TIME: 09:53:00

INPUT SET: S4679.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

0380
1800

SEQUENCE LISTING

ENTERED 4/23

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Goeddel, David V.
6 Rothe. Mike
7
8 (ii) TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
9
10 (iii) NUMBER OF SEQUENCES: 66
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: Genentech, Inc.
14 (B) STREET: 460 Point San Bruno Blvd
15 (C) CITY: South San Francisco
16 (D) STATE: California
17 (E) COUNTRY: USA
18 (F) ZIP: 94080
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: patin (Genentech)
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER:
28 (B) FILING DATE:
29 (C) CLASSIFICATION:
30
31 (vii) PRIOR APPLICATION DATA:
32 (A) APPLICATION NUMBER: 08/250858
33 (B) FILING DATE: 27-MAY-1994
34
35 (vii) PRIOR APPLICATION DATA:
36 (A) APPLICATION NUMBER: 08/331394
37 (B) FILING DATE: 28-OCT-1994
38
39 (viii) ATTORNEY/AGENT INFORMATION:
40 (A) NAME: Dreger, Ginger R.
41 (B) REGISTRATION NUMBER: 33,055
42 (C) REFERENCE/DOCKET NUMBER: 897P2
43
44 (ix) TELECOMMUNICATION INFORMATION:
45 (A) TELEPHONE: 415/225-3216
46 (B) TELEFAX: 415/952-9881

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47 (C) TELEX: 910/371-7168
48
49 (2) INFORMATION FOR SEQ ID NO:1:
50
51 (i) SEQUENCE CHARACTERISTICS:
52 (A) LENGTH: 2088 bases
53 (B) TYPE: nucleic acid
54 (C) STRANDEDNESS: single
55 (D) TOPOLOGY: linear
56
57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
58
59
60 CCCAGCCCGG TTCTCTGCCC CAAGGACGCT ACCGCCCAAT GCGAGCAGAA 50
61
62
63 GGCGGCGCAC AGATACAGAA AGTGAGGCTC AGACATATTG AAGACCGTGT 100
64
65
66 GACATAGGGT AGCCAAATGA CAGTGTGAGA AAGTGACATT TACTCAAGGC 150
67
68
69 CACCCAGATA TCCTGGAGGA CCCAGAACCC TGGAGATTCC CATCAGAAAG 200
70
71
72 ACCTTCTGGC CACCTGAAAC CCCAAGATGG CCTCCAGCTC AGCCCCTGAT 250
73
74
75 GAAAACGAGT TTCAATTTGG TTGCCCCCTT GCTCCCTGCC AGGACCCATC 300
76
77
78 GGAGCCCAGA GTTCTCTGCT GCACAGCCTG TCTCTCTGAG AACCTGAGAG 350
79
80
81 ATGATGAGGA TCGGATCTGT CCTAAATGCA GAGCAGACAA CCTCCATCCT 400
82
83
84 GTGAGCCCAG GAAGCCCTCT GACTCAGGAG AAGGTTCACT CTGATGTAGC 450
85
86
87 TGAGGCTGAA ATCATGTGCC CCTTTGCAGG TGTTGGCTGT TCCTTCAAGG 500
88
89
90 GGAGCCCACA ATCCATGCAG GAGCATGAGG CTACCTCCCA GTCCTCCAC 550
91
92
93 CTGTACCTGC TGCTGGCGGT CTTAAAGGAG TGGAAATCCT CACCAGGCTC 600
94
95
96 CAACCTAGGG TCTGCACCCA TGGCACTGGA GCGGAACCTG TCAGAGCTGC 650
97
98
99 AGCTTCAGGC AGCTGTGGAA GCGACAGGGG ACCTGGAGGT AGACTGCTAC 700

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100
101
102 CGGGCACCTT GCTGTGAGAG CCAGGAAGAA CTGGCCCTGC AGCACTTGGT 750
103
104
105 GAAGGAGAAG CTGCTGGCTC AGCTGGAGGA GAAGCTGCGT GTGTTTGCAA 800
106
107
108 ACATTGTTGC TGTCTCAAC AAGGAAGTGG AGGCTTCCCA CCTGGCACTG 850
109
110
111 GCCGCCTCCA TCCACCAGAG CCAGTTGGAC CGAGAGCACC TCCTGAGCTT 900
112
113
114 GGAGCAGAGG GTGGTGAAT TACAGCAAAC CCTGGCTCAA AAAGACCAGG 950
115
116
117 TCCTGGGCAA GCTTGAGCAC AGTCTGCGAC TCATGGAGGA GGCATCCTTT 1000
118
119
120 GATGGTACTT TCCTGTGGAA GATCACCAAT GTCACCAAGC GGTGCCACGA 1050
121
122
123 GTCAGTGTGT GGCCGGACTG TCAGCCTCTT CTCTCCAGCT TTCTACACTG 1100
124
125
126 CCAAGTATGG TTACAAGTTG TGCCTGCGCT TGTACCTGAA CGGGGATGGC 1150
127
128
129 TCAGGCAAGA AGACCCACCT GTCCCTCTTC ATCGTGATCA TGAGAGGAGA 1200
130
131
132 ATACGATGCT CTCCTGCCCT GGCCTTTCAG GAACAAGGTC ACCTTTATGC 1250
133
134
135 TACTTGACCA GAACAACCGA GAGCATGCTA TTGATGCCTT CCGGCCTGAC 1300
136
137
138 CTGAGCTCAG CCTCCTTCCA GCGGCCACAG AGTGAGACCA ACGTGGCCAG 1350
139
140
141 CGGCTGCCCC CTCTTCTTCC CCCTCAGCAA GCTGCAGTCA CCCAAGCACG 1400
142
143
144 CCTACGTCAA AGATGACACA ATGTTCTTCA AATGCATTGT GGACACTAGT 1450
145
146
147 GCTTAGGGAT GGGGGGAGGG GGTGTCTCCT GACAGAACCA GCTTAGACTG 1500
148
149
150 GGGGACTTAG CTAGACAGCC AGGCCCTGCC TGCCCTTGA GCCCACAGCC 1550
151
152

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153 CACGACAAGG AGGAGCCAAG GCTGGCATGA CTTGAGCGCC ACAGCATGCT 1600
154
155
156 GGTATATGGCT GATGTGAGGC TGGAGAAAACG TGTGCGTACA GAGACAGAGT 1650
157
158
159 GGAGGAGAAG ACAGAAGTGC TCTTTTCACA CAGACTACAC GACACCAGGA 1700
160
161
162 GGCCAGCATG CCAGCAGCTT CTGAATGTTG AGACCAGCCT AGATCAGGAT 1750
163
164
165 GAAAAGAGCC AGGCCTGAGG CTTGGACATT GAGCCAAGGC TATGGGGCCT 1800
166
167
168 AAGTGGAGGG GCACTCCTAC CAGGACATTC TCTCGAGGTC AGGGCATAAC 1850
169
170
171 TGGAAAAATG CCCCCATCTC TCTGTTTCAGA CTCAAAACTA GAACCACAGG 1900
172
173
174 GCAGAAGGGT CAGACATTAA TGTGAATTTA ACCTGCCCTG GACTGAGTTC 1950
175
176
177 CTATGTTAAC AGACACGCAA ACAGGTAAAC CCAGAAACTG CCCTGGGAAA 2000
178
179
180 TGCTTTCTGG CTGCATCTGG AGATCTTTGA TGTTTTTTACC GACAAAACAA 2050
181
182
183 ATAACAAAAG CCTTGAATTG CAAAAAAAAA AAAAAAAAAA 2088
184
185
186

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

190 (A) LENGTH: 409 amino acids
191 (B) TYPE: amino acid
192 (D) TOPOLOGY: linear
193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

194
195
196 Met Ala Ser Ser Ser Ala Pro Asp Glu Asn Glu Phe Gln Phe Gly
197 1 5 10 15
198
199 Cys Pro Pro Ala Pro Cys Gln Asp Pro Ser Glu Pro Arg Val Leu
200 20 25 30
201
202 Cys Cys Thr Ala Cys Leu Ser Glu Asn Leu Arg Asp Asp Glu Asp
203 35 40 45
204
205 Arg Ile Cys Pro Lys Cys Arg Ala Asp Asn Leu His Pro Val Ser

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206		50		55		60
207						
208	Pro Gly Ser Pro Leu Thr Gln Glu Lys Val His Ser Asp Val Ala					
209		65		70		75
210						
211	Glu Ala Glu Ile Met Cys Pro Phe Ala Gly Val Gly Cys Ser Phe					
212		80		85		90
213						
214	Lys Gly Ser Pro Gln Ser Met Gln Glu His Glu Ala Thr Ser Gln					
215		95		100		105
216						
217	Ser Ser His Leu Tyr Leu Leu Leu Ala Val Leu Lys Glu Trp Lys					
218		110		115		120
219						
220	Ser Ser Pro Gly Ser Asn Leu Gly Ser Ala Pro Met Ala Leu Glu					
221		125		130		135
222						
223	Arg Asn Leu Ser Glu Leu Gln Leu Gln Ala Ala Val Glu Ala Thr					
224		140		145		150
225						
226	Gly Asp Leu Glu Val Asp Cys Tyr Arg Ala Pro Cys Cys Glu Ser					
227		155		160		165
228						
229	Gln Glu Glu Leu Ala Leu Gln His Leu Val Lys Glu Lys Leu Leu					
230		170		175		180
231						
232	Ala Gln Leu Glu Glu Lys Leu Arg Val Phe Ala Asn Ile Val Ala					
233		185		190		195
234						
235	Val Leu Asn Lys Glu Val Glu Ala Ser His Leu Ala Leu Ala Ala					
236		200		205		210
237						
238	Ser Ile His Gln Ser Gln Leu Asp Arg Glu His Leu Leu Ser Leu					
239		215		220		225
240						
241	Glu Gln Arg Val Val Glu Leu Gln Gln Thr Leu Ala Gln Lys Asp					
242		230		235		240
243						
244	Gln Val Leu Gly Lys Leu Glu His Ser Leu Arg Leu Met Glu Glu					
245		245		250		255
246						
247	Ala Ser Phe Asp Gly Thr Phe Leu Trp Lys Ile Thr Asn Val Thr					
248		260		265		270
249						
250	Lys Arg Cys His Glu Ser Val Cys Gly Arg Thr Val Ser Leu Phe					
251		275		280		285
252						
253	Ser Pro Ala Phe Tyr Thr Ala Lys Tyr Gly Tyr Lys Leu Cys Leu					
254		290		295		300
255						
256	Arg Leu Tyr Leu Asn Gly Asp Gly Ser Gly Lys Lys Thr His Leu					
257		305		310		315
258						

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SEQUENCE VERIFICATION REPORT
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Error

Original Text